

SEQUENCE LISTING

<110> Jing, Shuqian

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<151> 2001-02-02

<150> US 09/723,232

<151> 2000-11-27

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<151> 2000-05-12

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Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys
515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val
530 535 540

Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
545 550 555 560

<210> 6
<211> 1713
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (273)..(1427)

<400> 6
ataaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcga tgctcgtcgt 60
gctgctaagc ctggccgcgc tgtgcaggag cgccgtaccc cgagagccga ccgttcaatg 120
tggctctgaa actgggccat ctccagagtg gatgctacaa catgatctaa tcccgggaga 180
cttgagggac ctccgagtag aacctgttac aactagtgtt gcaacagggg actattcaat 240
tttgatgaat gtaagctggg tactccgggc ag atg tgg aca ttt tcc tac atc 293
Met Trp Thr Phe Ser Tyr Ile
1 5

ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat	341
Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn	
10 15 20	
att cct aat gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat	389
Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn	
25 30 35	
ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag	437
Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys	
40 45 50 55	
tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag	485
Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys	
60 65 70	
aag aat gag gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga	533
Lys Asn Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly	
75 80 85	
aac aga tac atg gct ctt atc caa cac agc act atc atc ggg ttt tct	581
Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser	
90 95 100	
cag gtg ttt gag cca cac cag aag aaa caa acg cga gct tca gtg gtg	629
Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val	
105 110 115	
att cca gtg act ggg gat agt gaa ggt gct acg gtg cag ctg act cca	677
Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro	
120 125 130 135	
tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt	725
Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val	
140 145 150	
gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa	773
Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys	
155 160 165	
agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg	821
Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val	
170 175 180	
gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa	869
Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu	
185 190 195	
agg atc aag aag act tcc ttt tct acc acc aca cta ctg ccc ccc att	917
Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile	
200 205 210 215	
aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att	965
Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile	
220 225 230	
tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc	1013
Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile	
235 240 245	
ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag	1061
Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln	
250 255 260	

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tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt 1109
Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu
265 270 275

tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag 1157
Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu
280 285 290 295

ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac 1205
Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn
300 305 310

ctt ttc tgc agt gat cta aga agc cag att cat ctg cac aaa tac gtg 1253
Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val
315 320 325

gtg gtc tac ttt aga gag att gat aca aaa gac gat tac aat gct ctc 1301
Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu
330 335 340

agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt 1349
Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys
345 350 355

gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca 1397
Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser
360 365 370 375

caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccacccc atgagaagca 1447
Gln Ala Cys His Asp Gly Cys Cys Ser Leu
380 385

agagacctta aaggcttccct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga 1507

agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt 1567

ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc 1627

aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta accattttga 1687

taatgcaaca ataaagcatc ttcagc 1713

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<210> 7
 <211> 385
 <212> PRT
 <213> Homo sapiens

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<400> 7
Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val
1 5 10 15

Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp
20 25 30

Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His
35 40 45

Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp
50 55 60

Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn
65 70 75 80

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Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His
85 90 95

Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys
100 105 110

Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly
115 120 125

Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys
130 135 140

Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro
145 150 155 160

Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu
165 170 175

Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile
180 185 190

Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr
195 200 205

Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu
210 215 220

Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn
225 230 235 240

His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile
245 250 255

Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala
260 265 270

Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp
275 280 285

Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp
290 295 300

Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln
305 310 315 320

Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr
325 330 335

Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met
340 345 350

Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln
355 360 365

Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser
370 375 380

Leu
385

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2429-59

<400> 8
gcagacactg agagcattgt aatcg 25

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
1916-83

<400> 9
ggctcgtatg ttgtgtggaa ttgtgag 27

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2429-56

<400> 10
atcaagaaga cttccttttc tac 23

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 1916-80

<400> 11
tgcaaggcga ttaagttggg taacgccag 29

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nested PCR
Primer

<400> 12
gccgacgggg acgtggatga ac 22

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nested PCR
Primer

<400> 13
catgattacg ccaagctcta atacgactc 29

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nested PCR
Primer

<400> 14
cttcgccgag tgcctgtgca g 21

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nest PCR
Primer

<400> 15
tcacgacgtt gtaaaacgac ggccagtg 28

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2469-50

<400> 16
gcgatgtcgc tcgtgctgct aag 23

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2469-54

<400> 17
gcagcctggg gaggtgaaat tcac 24

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 18
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 19
Phe Ile Thr Cys Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg
1 5 10 15

Arg Arg

<210> 20
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epogen signal
peptide

<400> 20
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
20 25

<210> 21
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide of Fc
fragment

<400> 21
Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30


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tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272
Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp
      25                      30                      35

agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320
Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His
      40                      45                      50

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc 368
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala
      55                      60                      65                      70

atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc 416
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro
      75                      80                      85

cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta 464
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu
      90                      95                      100

cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac 512
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr
      105                      110                      115

cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag gcc 560
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly
      120                      125                      130

acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta 608
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu
      135                      140                      145                      150

gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag 644
Ala Cys Val Cys Val Arg Pro Arg Val Met Gly
      155                      160

<210> 23
<211> 161
<212> PRT
<213> Homo sapiens

<400> 2
Met Tyr Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr His Thr
  1                      5                      10                      15

Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser
      20                      25                      30

Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
      35                      40                      45

Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
      50                      55                      60

Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
      65                      70                      75                      80

Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
      85                      90                      95

Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
      100                      105                      110

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CCDS: 260765.1

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<210> 24
<211> 521
<212> PRT
<213> Homo sapiens
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<400>	23															
Met	Ser	Leu	Val	Leu	Leu	Ser	Leu	Ala	Ala	Leu	Cys	Arg	Ser	Ala	Val	
1				5					10					15		
Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro	
			20					25					30			
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu	
		35					40					45				
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile	
	50					55					60					
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu	
65					70					75					80	
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	
				85					90					95		
Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	Glu	Ala	Phe	Gln	Thr	Gln	Ser	
			100					105					110			
Gly	Gly	Lys	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	
		115					120					125				
Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	
	130					135					140					
Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	
145					150					155					160	
Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	
				165					170					175		
Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	
			180					185					190			
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	
		195					200					205				
Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	
	210					215					220					
Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	
225					230					235					240	

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys
580 585

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

cattttccta catcggttc cctg

24

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 27
tgaatctggc ttctttcact gc

22

ttctttcact gc